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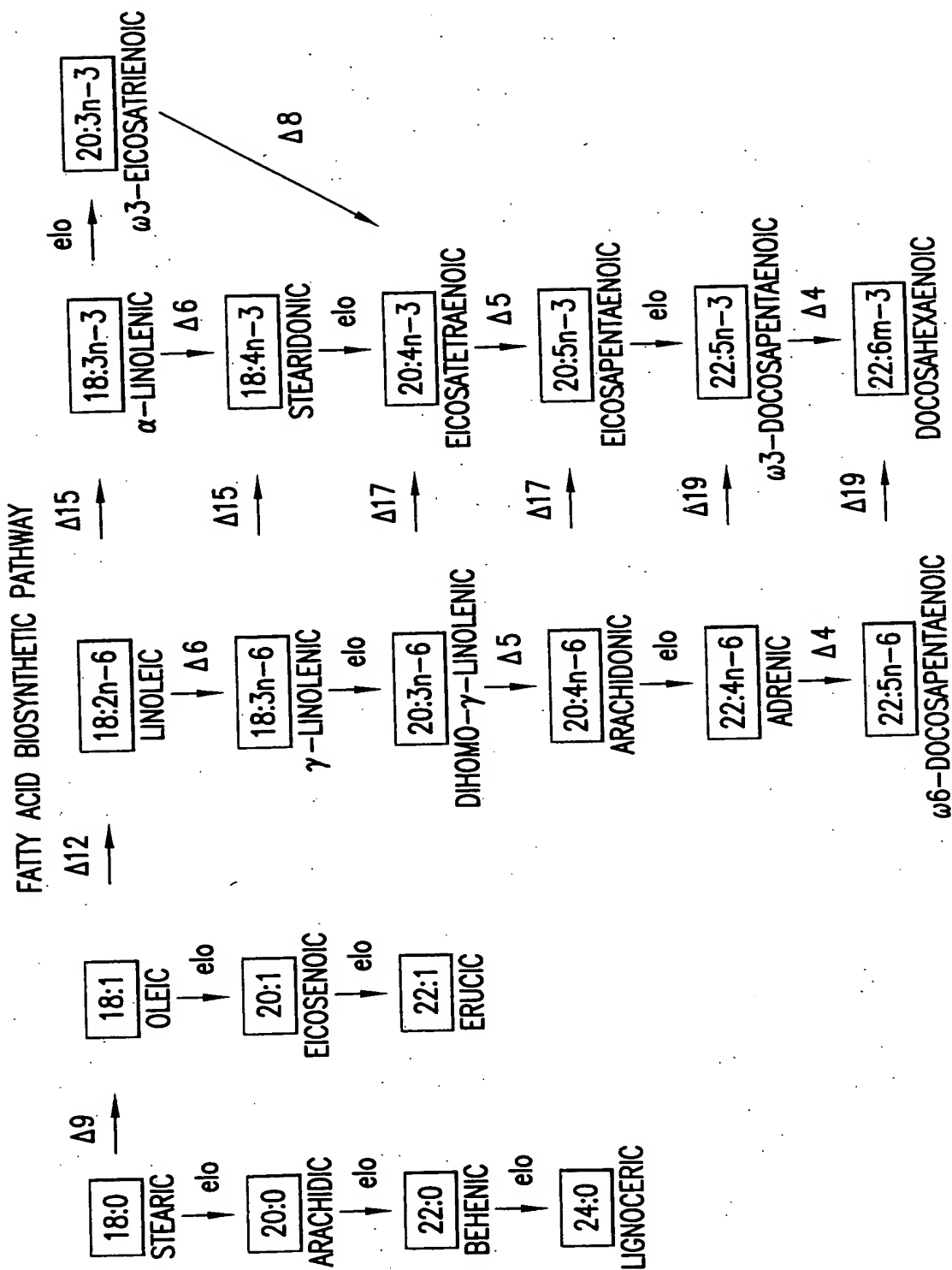


FIG.1

Gene Sequence of *sdd17*, an Omega-3 Fatty Acid Desaturase Gene
from *Saprolegnia diclina* (ATCC 56851)

```

 1 ATGACTGAGG ATAAGACGAA GGTGAGTTC CCGACGCTCA CGGAGCTCAA
51 GCACTCGATC CCGAACGCGT GCTTTGAGTC GAACCTCGGC CTCTCGCTCT
101 ACTACACGGC CCGCGCGATC TTCAACGCGT CGGCCTCGGC GGCGCTGCTC
151 TACGCGGCGC GCTCGACGCC GTTCATTGCC GATAACGTTT TGCTCCACGC
201 GCTCGTTTGC GCCACCTACA TCTACGTGCA GGGCGTCATC TTCTGGGGCT
251 TCTTCACGGT CGGCCACGAC TGCGGCCACT CGGCCTTCTC GCGCTACCAC
301 AGCGTCAACT TTATCATCGG CTGCATCATG CACTCTGCGA TTTTGACGCC
351 GTTCGAGAGC TGGCGCGTGA CGCACCGCCA CCACCACAAG AACACGGGCA
401 ACATTGATAA GGACGAGATC TTTTACCGC ACCGGTCGGT CAAGGACCTC
451 CAGGACGTGC GCCAATGGGT CTACACGCTC GGCGGTGCGT GGTTCGTCTA
501 CTTGAAGGTC GGGTATGCCC CGCGCACGAT GAGCCACTTT GACCCGTGGG
551 ACCCGCTCCT CTTTCGCCGC GCGTCGGCCG TCATCGTGTC GCTCGGCGTC
601 TGGGCCGCCT TCTTCGCCGC GTACGCGTAC CTCACATACT CGCTCGGCTT
651 TGCCGTCATG GGCCTCTACT ACTATGCGCC GCTCTTTGTC TTTGCTTCGT
701 TCCTCGTCAT TACGACCTTC TTGCACCACA ACGACGAAGC GACGCCGTGG
751 TACGGCGACT CGGAGTGGAC GTACGTCAAG GGCAACCTCT CGAGCGTCGA
801 CCGCTCGTAC GGCGCGTTTC TGGACAACCT GAGCCACCAC ATTGGCACGC
851 ACCAGGTCCA CCACTTGTTT CCGATCATTG CGCACTACAA GCTCAACGAA
901 GCCACCAAGC ACTTTGCGGC CGCGTACCCG CACCTCGTGC GCAGGAACGA
951 CGAGCCCATC ATCACGGCCT TCTTCAAGAC CGCGCACCTC TTTGTCAACT
1001 ACGGCGCTGT GCCCGAGACG GCGCAGATCT TCACGCTCAA AGAGTCGGCC
1051 GCGGCCGCCA AGGCCAAGTC GGAATAA

```

FIG.2

Amino Acid Sequence of an Omega-3 Fatty Acid Desaturase (SDD17) from
Saprolegnia diclina (ATCC 56851)

1 MTEDKTKVEF PTLTELKHSI PNACFESNLG LSLYYTARAI FNASASAALL
51 YAARSTPFIA DNVLLHALVC ATYIYVQGVI FWGFFTVGHD CGHSAFSRYH
101 SVNFIIGCIM HSAILTPFES WRVTHRHHHK NTGNIDKDEI FYPHRSVKDL
151 QDVRQWVYTL GGAWFVYLKV GYAPRTMSHF DPWDPLLLRR ASAVIVSLGV
201 WAAFFAAYAY LTYSLGFAVM GLYYYAPLFV FASFLVITTF LHHNDEATPW
251 YGDSEWTVVK GNLSSVDRSY GAFVDNLSSH IGTHQVHHLF PIIPHYKLNE
301 ATKHFAAAYP HLVRRNDEPI ITAFFKTAHL FVNYGAVPET AQIFTLKESA
351 AAAKAKSD*

FIG.3

Comparative analysis of *S. diclina* Delta 17-desaturase (SDD17.pep)
& *Synechocystis* sp. Delta 15-desaturase (SYCDESB)

Frame: 2 initn: 733 initl: 305 opt: 689 Z-score: 996.8 expect(): 1.5e-47
40.9% identity in 269 aa overlap
(76-336:204-471)

	50	60	70	80	90	100
SDD17.pep	SAALLYAARSTPFIADNVLLHALVCATYIYVQGVIFWGFFT	VGHDCGHS	AFSRYHSVNFI			
SYCDESB	YFFLDVGLIAGFYALAA	YLDSWFFYP	IFWLIQGT	LFWSLFVVG	HDCGHSFS	SKSKTLNN
	530	560	590	620	650	680
	110	120	130	140	150	160
SDD17.pep	IGCIMHSAILTPFESWRV	THRHHKNTGNIDK	DEIFYPHRSVKDLQ	----	DVRQWVYT	LG
		:	:	:	:	:
SYCDESB	IGHLSHTPILVPYHGR	ISHRTHHANTGNID	TDES	WYPVSEQYNQMA	WYEKLLRFY	LPL
	710	740	770	800	830	860
	170	180	190	200	210	220
SDD17.pep	GAWFVYLKVGYPRTMS	HFDPLLL-RRAS	AVIVSLGVWAA	FFAAYALT	YSLGFAVM	
		:	:	:	:	:
SYCDESB	IAYPIYLFRRSPNR	QGSHPGSP	FRPGEKA	AVLTSTFALA	AFVGLGFLT	WQFGWLFL
	890	920	950	980	1010	1040
	230	240	250	260	270	280
SDD17.pep	GLYYYAPLFVFASFL	VITTF	LHND	EATPWYGD	SEWTVKGNL	SSVDRSYGAFVDNL
	:	:	:	:	:	:
SYCDESB	LKFYVAPYLVFVW	LDLVTFLH	HTEDNIPWYR	GDDWYFLK	GALSTIDR	DYG-FINPIHHD
	1070	1100	1130	1160	1190	1220
	290	300	310	320	330	
SDD17.pep	IGTHQVHHLFPIIPHY	KLNEATKHFAA	AYPHLVRRNDE	PIITAFFKT	----	AHLFVNYGAV
		:	:	:	:	:
SYCDESB	IGTHVAHHIFSNM	PHYKLRRATEA	IKPILGEY	YRYSDEPIWQ	AFFKSYWACH	FVPNQSG
	1250	1280	1310	1340	1370	1400
	340	350				
SDD17.pep	PETAQIFTLKES	AAAAKAKSD				
SYCDESB	VYYQSPSNGGYQ	KKPXLILIES	NQHREG	RQYXMVLL	PSDRLMR	SMEEVKQSHSKRSALNQ
	1430	1460	1490	1520	1550	1580

FIG.4

Frame: 1 initn: 490 init1: 222 opt: 502 Z-score: 724.0 expect(): 2.3e-32
31.6% identity in 310 aa overlap
(2-303:49-347)

[illegible]

FIG. 5

Gene Sequence of *sdd12*, a Delta 12-Desaturase Gene
from *Saprolegnia diclina* (ATCC 56851)

```

1  ATGTGCAAAG GTCAAGCTCC TTCCAAGGCC GACGTGTTCC ACGCTGCGGG
51  GTACCGCCCG GTCGCCGGCA CGCCCGAGCC GCTGCCGCTG GAGCCCCCGA
101 CGATCACGCT CAAGGACCTG CGCGCGGCGA TCCCGGCCCA CTGCTTTGAG
151 CGCAGCGCTG CCACTAGCTT TTACCATTTG GCCAAGAACC TTGCGATCTG
201 CGCCGGCGTG TTCGCCGTTG GCCTCAAGCT CGCGGCTGCC GACTTGCCGC
251 TCGCGGCCAA GCTGGTCGCG TGGCCCATCT ACTGGTTCGT CCAGGGCACG
301 TACTTTACGG GCATCTGGGT CATTGCGCAC GAATGCGGCC ACCAGGCGTT
351 CTCGGCGTCC GAGATCCTCA ACGACACGGT CGGTATCATT CTTCACTCGC
401 TCCTCTTTGT GCCGTACCAC AGCTGGAAGA TCACGCACCG CCGCCACCAC
451 TCCAACACGG GCAGCTGCCA GAACGACGAG GTGTTTACGC CGACGCCGCG
501 GTCCGTCGTC GAGGCCAAGC ACGACCACTC GTCCTCGAA GAGAGCCCGC
551 TCTACAACCT GTACGGCATC GTCATGATGC TTCTCGTGGG CTGGATGCCG
601 GGCTACCTCT TCTTCAACGC GACCGGCCCG ACCAAGTACG CTGGCCTCGC
651 CAAGTCGCAC TTCAACCCGT ACGCAGCCTT TTTCTCCCA AAGGAGCGCC
701 TCAGCATCTG GTGGAGCGAC CTCTGCTTCC TCGCGGCCTT GTACGGCTTT
751 GGCTACGGCG TCTCGGTCTT CGGCCTCCTC GATGTCGCCC GCCACTACAT
801 CGTGCCGTAC CTCATTTGCA ACGCGTACCT CGTGCTCATC ACGTACCTCC
851 AGCACACGGA TACGTACGTG CCCCCTTCC GCGGCGACGA GTGGAAGTGG
901 CTGCGCGGCG CGCTCTGCAC CGTCGACCGC TCGTTCGGCG CGTGGATCGA
951 CAGCGCGATC CACCACATTG CCGACACGCA CGTGACGCAC CACATTTTCT
1001 CCAAGACGCC CTTCTACCAC GCGATCGAGG CGACCGACGC CATCACGCCC
1051 CTCCTCGGCA AGTACTACCT CATCGACCCG ACGCCGATCC CGCTGGCGCT
1101 CTGGCGCTCG TTCACGCACT GCAAGTACGT CGAGGACGAC GGCAACGTTG
1151 TGTTTTACAA GCGCAAGCTC GAGGAAAAGT AA

```

FIG.6

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Amino Acid Sequence of α Delta 12-Desaturase (SDD12) from *Saprolegnia diclina* (ATCC 56851)

```
1  MCKGQAPSKA DVFHAAGYRP VAGTPEPLPL EPPTITLKDL RAAIPAHCFE
51  RSAATSFYHL AKNLAICAGV FAVGLKLAAL DLPLAAKLVA WPIYWFVQGT
101 YFTGIWVIAH ECGHQAFSAS EILNDTVGII LHSLLFVPYH SWKITHRRHH
151 SNTGSCENDE VFTPTPRSVV EAKHDHSLLE ESPLYNLYGI VMMLLVGWMP
201 GYLFFNATGP TKYAGLAKSH FNPYAAFFLP KERLSIWWSL LCFLAALYGF
251 GYGVSFVGLL DVARHYIVPY LICNAYLVLI TYLQHTDTYV PHFRGDEWNW
301 LRGALCTVDR SFGAWIDSAI HHIADTHVTH HIFSKTPFYH AIEATDAITP
351 LLGKYLLIDP TPIPLALWRS FTHCKYVEDD GNVVFYKRKL EEK*
```

FIG.7

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Comparative analysis of *S. diclina* Delta 12-desaturase (SDD12.pep)
& *G. hirsutum* Delta 12-desaturase (GH06DES)

Frame: 3 initn: 992 init1: 413 opt: 1086 Z-score: 1531.8 expect(): 2.3e-77
45.6% identity in 379 aa overlap
(9-380:14-384)

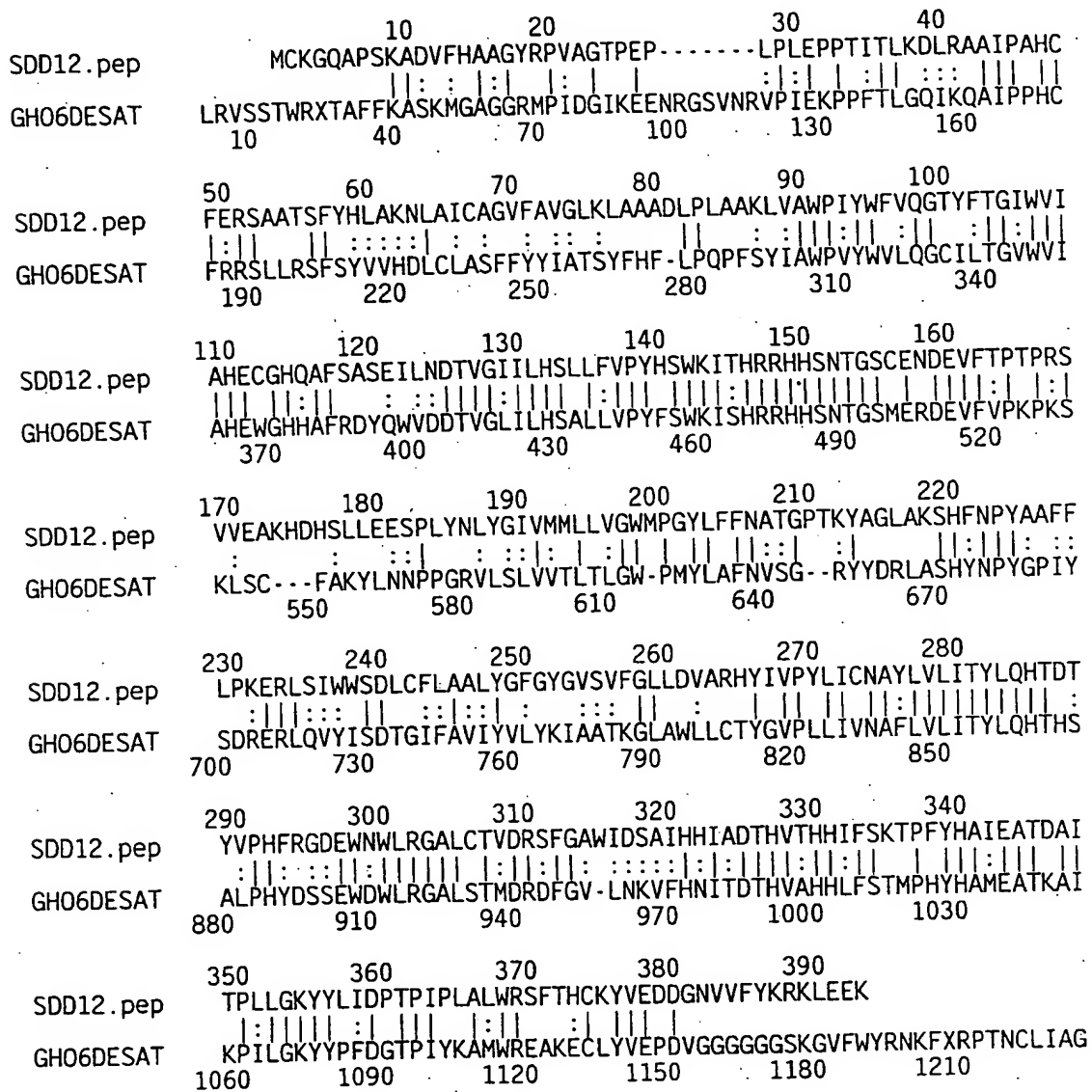


FIG.8

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Sequence ID:

Sequence ID 1

5'-ATC CGC GCC GCC ATC CCC AAG CAC TGC TGG GTC AAG-3'

Sequence ID 2

5'-GCC CTC TTC GTC CTC GGC CAY GAC TGC GGC CAY GGC TCG TTC TCG-3'

Sequence ID 3

5'-GAG RTG GTA RTG GGG GAT CTG GGG GAA GAR RTG RTG GRY GAC RTG-3'

Sequence ID 4

5'-CCC TAC CAY GGC TGG CGC ATC TCG CAY CGC ACC CAY CAY CAG AAC-3'

Sequence ID 5

5'-GTT CTG RTG RTG GGT CCG RTG CGA GAT GCG CCA GCC RTG GTA GGG-3'

Sequence ID 6

5'-GGC TCG CAC TTC SAC CCC KAC TCG GAC CTC TTC GTC-3'

Sequence ID 7

5'-GAC GAA GAG GTC CGA GTM GGG GTW GAA GTG CGA GCC-3''

Sequence ID 8

5'-GCG CTG GAK GGT GGT GAG GCC GCC GCG GAW GSA CGA CCA-3'

Sequence ID 9

5'-CTG GGG GAA GAG RTG RTG GAT GAC RTG GGT GCC GAT GTC RTG RTG-3'

Sequence ID 10

5'-GGT GGC CTC GAY GAG RTG GTA RTG GGG GAT CTK GGG GAA GAR RTG-3'

Sequence ID 11

5'-GAG RTG GTA RTG GGG GAT CTG GGG GAA GAR RTG RTG GRY GAC RTG-3'

Sequence ID 12

5'-TAC GCG TAC CTC ACG TAC TCG CTC G-3'

Sequence ID 13

5'-TTC TTG CAC CAC AAC GAC GAA GCG ACG-3'

Sequence ID 14

5'-GGA GTG GAC GTA CGT CAA GGG CAA C-3'

Sequence ID 15

5'-TCA AGG GCA ACC TCT CGA GCG TCG AC-3'

Sequence ID 16

5'-CCC AGT CAC GAC GTT GTA AAA CGA CGG CCA G-3'

FIG.9A

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Sequence ID 17

5'-AGC GGA TAA CAA TTT CAC ACA GGA AAC AGC -3'

Sequence ID 18

5'-GGT AAA AGA TCT CGT CCT TGT CGA TGT TGC-3'

Sequence ID 19

5'-GTC AAA GTG GCT CAT CGT GC-3'

Sequence ID 20

5'-CGA GCG AGT ACG TGA GGT ACG CGT AC-3'

Sequence ID 21

5'-TCA ACA GAA TTC ATG ACC GAG GAT AAG ACG AAG GTC GAG TTC CCG-3'

Sequence ID 22

5'-AAA AGA AAG CTT CGC TTC CTA GTC TTA GTC CGA CTT GGC CTT GGC-3'

Sequence ID 23

5'-TCA ACA AAG CTT ATG ACC GAG GAT AAG ACG AAG GTC GAG TTC CCG-3'

Sequence ID 24

5'-AAA AGA GAA TTC CGC TTC CTA GTC TTA GTC CGA CTT GGC CTT GGC-3'

Sequence ID 25

```
1  ATGACTGAGG ATAAGACGAA GGTCTGAGTTC CCGACGCTCA CGGAGCTCAA
51  GCACTCGATC CCGAACGCGT GCTTTGAGTC GAACCTCGGC CTCTCGCTCT
101 ACTACACGGC CCGCGCGATC TTCAACGCGT CGGCCTCGGC GGCCTGCTC
151 TACGCGGCGC GCTCGACGCC GTTCATTGCC GATAACGTTT TGCTCCACGC
201 GTCGTTTTGC GCCACCTACA TCTACGTGCA GGGCGTCATC TTCTGGGGCT
251 TCTTCACGGT CGGCCACGAC TGCGGCCACT CGGCCTTCTC GCGCTACCAC
301 AGCGTCAACT TTATCATCGG CTGCATCATG CACTCTGCGA TTTTGACGCC
351 GTTCGAGAGC TGGCGCGTGA CGCACCGCCA CCACCACAAG AACACGGGCA
401 ACATTGATAA GGACGAGATC TTTTACCCGC ACCGGTCGGT CAAGGACCTC
451 CAGGACGTGC GCCAATGGGT CTACACGCTC GGCGGTGCCT GGTTCGTCTA
501 CTTGAAGGTC GGGTATGCCC CGCGCACGAT GAGCCACTTT GACCCGTGGG
551 ACCCGCTCCT CTTTCGCCGC GCGTCGGCCG TCATCGTGTC GCTCGGCGTC
601 TGGGCCGCCCT TCTTCGCCGC GTACGCGTAC CTCACATACT CGCTCGGCTT
651 TGCCGTGTCG GGCCTCTACT ACTATGCGCC GCTCTTTGTC TTTGCTTCGT
701 TCCTCGTCAT TACGACCTTC TTGCACCACA ACGACGAAGC GACGCCGTGG
751 TACGGCGACT CGGAGTGGAC GTACGTCAAG GGCAACCTCT CGAGCGTCGA
801 CCGCTCGTAC GGCAGGTTCC TGGACAACCT GAGCCACCAC ATTGGCACGC
851 ACCAGGTCCA CCACTTGTTT CCGATCATTG CGCACTACAA GCTCAACGAA
901 GCCACCAAGC ACTTTGCGGC CGCGTACCCG CACCTCGTGC GCAGGAACGA
951 CGAGCCCATC ATCACGGCCT TCTTCAAGAC CGCGCACCTC TTTGTCAACT
1001 ACGGCGCTGT GCCCGAGACG GCGCAGATCT TCACGCTCAA AGAGTCGGCC
1051 GCGGCCGCCA AGGCCAAGTC GGAATAA
```

FIG.9B

Sequence ID 26

```

1  MTEDKTKVEF PTLTELKHSI PNACFESNLG LSLYYTARAI FNASASAALL
51  YAARSTPFIA DNVLLHALVC ATYIYVQGVI FWGFFTGVHD CGHSAFSRYH
101 SVNFIIGCIM HSAILTPFES WRVTHRHHHK NTGNIDKDEI FYPHRSVKDL
151 QDVRQWVYTL GGAWFVYLKV GYAPRTMSHF DPWDPLLLRR ASAVIVSLGV
201 WAAFFAAYAY LTYSLGFAVM GLYYYAPLFV FASFLVITTF LHHNDEATPW
251 YGDSEWTVYK GNLSSVDRSY GAFVDNLSSH IGTHQVHHLF PIIPHYKLNE
301 ATKHFAAAYP HLVRNDEPI ITAFFKTAHL FVNYGAVPET AQIFTLKESA
351 AAAKAKSD*

```

Sequence ID 27

```

1  ATGGCCCCGC AGACGGAGCT CCGCCAGCGC CACGCCGCCG TCGCCGAGAC
51  GCCGGTGGCC GGCAAGAAGG CCTTTACATG GCAGGAGGTC GCGCAGCACA
101 ACACGGCGGC CTCGGCCTGG ATCATTATCC GCGGCAAGGT CTACGACGTG
151 ACCGAGTGGG CCAACAAGCA CCCCGGCGGC CGCGAGATGG TGCTGCTGCA
201 CGCCGGTCGC GAGGCCACCG ACACGTTCTGA CTCGTACCAC CCGTTCAGCG
251 ACAAGGCCGA GTCGATCTTG AACAAGTATG AGATTGGCAC GTTCACGGGC
301 CCGTCCGAGT TTCCGACCTT CAAGCCGGAC ACGGGCTTCT ACAAGGAGTG
351 CCGCAAGCGC GTTGGCGAGT ACTTCAAGAA GAACAACCTC CATCCGCAGG
401 ACGGCTTCCC GGGCCTCTGG CGCATGATGG TCGTGTTTGC GGTGCGCGGC
451 CTCGCCTTGT ACGGCATGCA CTTTTCGACT ATCTTTGCGC TGCAGCTCGC
501 GGCCGCGGCG CTCTTTGGCG TCTGCCAGGC GCTGCCGCTG CTCCACGTCA
551 TGCACGACTC GTCGCACGCG TCGTACACCA ACATGCCGTT CTTCCATTAC
601 GTCGTCGGCC GCTTTGCCAT GGACTGGTTT GCCGGCGGCT CGATGGTGTC
651 ATGGCTCAAC CAGCACGTCG TGGGCCACCA CATCTACAG AACGTCGCG
701 GCTCGGACCC GGATCTTCCG GTCAACATGG ACGGCGACAT CCGCCGCATC
751 GTGAACCGCC AGGTGTTCCA GCCCATGTAC GCATTCCAGC ACATCTACCT
801 TCCGCCGCTC TATGGCGTGC TTGGCCTCAA GTTCCGCATC CAGGACTTCA
851 CCGACACGTT CGGCTCGCAC ACGAACGGCC CGATCCGCGT CAACCCGCAC
901 GCGCTCTCGA CGTGGATGGC CATGATCAGC TCCAAGTCGT TCTGGGCCTT
951 CTACCGCGTG TACCTTCCGC TTGCCGTGCT CCAGATGCCC ATCAAGACGT
1001 ACCTTGCGAT CTTCTTCCTC GCCGAGTTTG TCACGGGCTG GTACCTCGCG
1051 TTCAACTTCC AAGTAAGCCA TGTCTCGACC GAGTGCGGCT ACCCATGCGG
1101 CGACGAGGCC AAGATGGCGC TCCAGGACGA GTGGGCAGTC TCGCAGGTCA
1151 AGACGTCGGT CGACTACGCC CATGGCTCGT GGATGACGAC GTTCCTTGCC
1201 GGCGCGCTCA ACTACCAGGT CGTGACCAC TTGTTCCCA GCGTGTCGCA
1251 GTACCACTAC CCGGCGATCG CGCCATCAT CGTCGACGTC TGCAAGGAGT
1301 ACAACATCAA GTACGCCATC TTGCCGGACT TTACGGCGGC GTTCGTTGCC
1351 CACTTGAAGC ACCTCCGCAA CATGGGCCAG CAGGGCATCG CCGCCACGAT
1401 CCACATGGGC TAA

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FIG.9C

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Sequence ID 28

```
1  ATGGCAAACA GCAGCGTGTG GGATGATGTG GTGGGCCGCG TGGAGACCGG
51  CGTGGACCAG TGGATGGATG GCGCCAAGCC GTACGCACTC ACCGATGGGC
101 TCCCGATGAT GGACGTGTCC ACCATGCTGG CATTGAGGT GGGATACATG
151 GCCATGCTGC TCTTCGGCAT CCCGATCATG AAGCAGATGG AGAAGCCTTT
201 TGAGCTCAAG ACCATCAAGC TCTTGACAA CTTGTTTCTC TTCGGACTTT
251 CTTGTACAT GTGCGTGGAG ACCATCCGCC AGGCTATCCT CGGAGGCTAC
301 AAAGTGTGTTG GAAACGACAT GGAGAAGGGC AACGAGTCTC ATGCTCAGGG
351 CATGTCTCGC ATCGTGTACG TGTTCTGCGT GTCCAAGGCA TACGAGTTCT
401 TGGATACCGC CATCATGATC CTTTGCAAGA AGTTCAACCA GGTTCCTTC
451 TTGCATGTGT ACCACCATGC CACCATTTTT GCCATCTGGT GGGCTATCGC
501 CAAGTACGCT CCAGGAGGTG ATGCGTACTT TTCAGTGATC CTCAACTCTT
551 TCGTGCACAC CGTCATGTAC GCATACTACT TCTTCTCCTC CCAAGGGTTC
601 GGGTTCGTGA AGCCAATCAA GCCGTACATC ACCACCCTTC AGATGACCCA
651 GTTCATGGCA ATGCTTGTGC AGTCCTTGTA CGACTACCTC TTCCCATGCG
701 ACTACCCACA GGCTCTTGTG CAGCTTCTTG GAGTGTACAT GATCACCTTG
751 CTTGCCCTCT TCGGCAACTT TTTTGTGCAG AGCTATCTTA AAAAGCCAAA
801 AAAGAGCAAG ACCAACTAA
```

Sequence ID 29

```
1  MTVGFDETVT MDTVRNHNMP DDAWCAIHGT VYDITKFSKV HPGGDIIMLA
51  AGKEATILFE TYHIKGVPA VLRKYKVGKL PQGKKGETSH MPTGLDSASY
101 YSWDSEFYRV LRERVAKKLA EPGLMQRARM ELWAKAIFLL AGFWGSLYAM
151 CVLDPHGGAM VAAVTLGVFA AFVGTCTIQHD GSHGAFSKSR FMNKAAGWTL
201 DMIGASAMTW EMQHVLGHHY YTNLIEMENG LAKVKGADVD PKKVDQESDP
251 DVFSTYPLMR LHPWHRQRFY HKFQHLIYAPL IFGFMINKV ISQDVGVLRL
301 KRLFQIDANC RYGSPWNVAR FWIMKLLTTL YMVALPMMQ GPAQGLKLFF
351 MAHFTCGEVL ATMFIWNHII EGVSYASKDA VKGVMAPPRT VHGVTPMQVT
401 QKALSAAEST KSDADKTTMI PLNDWAAVQC QTSVNWAVGS WFWNHFSGLL
451 NHQIEHCFP QNPHTVNVYI SGIVKETCEE YGVPIYQAEIS LFSAYFKMLS
501 HLRTLGNEDL TAWST*
```

Sequence ID 30

5'-CCG SAG TTC ACS ATC AAG GAG ATC CGC GAS KSC ATC CCG GCC CAC TGC TTC -3'

Sequence ID 31

5'-GRS CTT CTT GAK GTG GWM SGT GGC CTC CTC GGC GTG GTA GWR CGG CAT-3'

Sequence ID 32

5'-CCS STC TAC TGG GCC TGC CAG GGT RTC GTC CTC ACS GGT GTC TGG-3'

FIG.9D

Sequence ID 33

5'-CCS STC TAC TGG ATC RYS CAG GGT RTC GTC KGY ACS GGT GTC TGG-3'

Sequence ID 34

5'-GGC GTG GTA GTG CGG CAT SMM CGA GAA GAR GTG GTG GGC GAC GTG-3'

Sequence ID 35

5'-CAC GTA CCT CCA GCA CAC GGA CAC CTA CG-3'

Sequence ID 36

5'-GAT CGA CAG CGC GAT CCA CCA CAT TGC-3'

Sequence ID 37

5'-CAA ATG GTA AAA GCT AGT GGC AGC GCT GC-3'

Sequence ID 38

5'-AGT ACG TGC CCT GGA CGA ACC AGT AGA TG-3'

Sequence ID 39

5'-TCA ACA GAA TTC ATG TGC AAA GGT CAA GCT CCT TCC AAG GCC GAC GTG -3'

Sequence ID 40

5'-AAA AGA AAG CTT TTA CTT TTC CTC GAG CTT GCG CTT GTA AAA CAC AAC-3'

Sequence ID 41

```

1  ATGTGCAAAG GTCAAGCTCC TTCCAAGGCC GACGTGTTCC ACGCTGCGGG
51  GTACCGCCCG GTCGCCGGCA CGCCCGAGCC GCTGCCGCTG GAGCCCCCGA
101 CGATCACGCT CAAGGACCTG CGCGCGGCGA TCCCGGCCCA CTGCTTTGAG
151 CGCAGCGCTG CCACTAGCTT TTACCATTG GCCAAGAACC TTGCGATCTG
201 CGCCGGCGTG TTCGCCGTTG GCCTCAAGCT CGCGGCTGCC GACTTGCCGC
251 TCGCGGCCAA GCTGGTCGCG TGGCCCATCT ACTGGTTCGT CCAGGGCAGC
301 TACTTTACGG GCATCTGGGT CATTGCGCAC GAATGCGGCC ACCAGGCGTT
351 CTCGGCGTCC GAGATCCTCA ACGACACGGT CGGTATCATT CTTCACTCGC
401 TCCTCTTTGT GCCGTACCAC AGCTGGAAGA TCACGCACCG CCGCCACCAC
451 TCCAACACGG GCAGCTGCGA GAACGACGAG GTGTTTACGC CGACGCCGCG
501 GTCCGTGCTC GAGGCCAAGC ACGACCACTC GCTCCTCGAA GAGAGCCCGC
551 TCTACAACCT GTACGGCATC GTCATGATGC TTCTCGTGGG CTGGATGCCG
601 GGCTACCTCT TCTTCAACGC GACCGGCCCG ACCAAGTACG CTGGCCTCGC
651 CAAGTCGCAC TTCAACCCGT ACGCAGCCTT TTTCTCCCA AAGGAGCGCC
701 TCAGCATCTG GTGGAGCGAC CTCTGCTTCC TCGCGGCCTT GTACGGCTTT
751 GGCTACGGCG TCTCGGTCTT CGGCCTCCTC GATGTCGCC GCCACTACAT
801 CGTGCCGTAC CTCATTTGCA ACGGTACCT CGTGCTATC ACGTACCTCC
851 AGCACACGGA TACGTACGTG CCCCATTCC GCGGCGACGA GTGGAAGTGG
901 CTGCGCGGCG CGCTCTGCAC CGTCGACCGC TCGTTCGGCG CGTGGATCGA
951 CAGCGCGATC CACCACATTG CCGACACGCA CGTGACGCAC CACATTTTCT
1001 CCAAGACGCC CTTCTACCAC GCGATCGAGG CGACCGACGC CATCACGCC
1051 CTCCTCGGCA AGTACTACCT CATCGACCG ACGCCGATCC CGCTGGCGCT
1101 CTGGCGCTCG TTCACGCACT GCAAGTACGT CGAGGACGAC GGCAACGTTG
1151 TGTTTTACAA GCGCAAGCTC GAGGAAAAGT AA

```

FIG.9E

Sequence ID 42

1 MCKGQAPSKA DVFHAAGYRP VAGTPEPLPL EPPTITLKDL RAAIPAHCFE
51 RSAATSFYHL AKNLAICAGV FAVGLKLAAL DLPLAAKLVA WPIYWFVQGT
101 YFTGIWVIAH ECGHQAFSAS EILNDTVGII LHSLLFVPYH SWKITHRRHH
151 SNTGSCENDE VFTPTPRSVV EAKHDHSLLE ESPLYNLYGI VMMLLVGWMP
201 GYLFFNATGP TKYAGLAKSH FNPYAAFFLP KERLSIWWSL LCFLAALYGF
251 GYGVSVFGLL DVARHYIVPY LICNAYLVL I TYLQHTDTYV PHFRGDEWNW
301 LRGALCTVDR SFGAWIDSAI HHIADTHVTH HIFSKTPFYH AIEATDAITP
351 LLGKYYLIDP TPIPLALWRS FTHCKYVEDD GNVVFYKRKL EEK*

FIG.9F